

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 10, 1999, 06:14:03 ; Search time 9.95 Seconds  
(without alignments)  
488.658 Million cell updates/sec

Title: US-09-208-619-1  
Perfect score: 911  
Sequence: 1 MEEYAREPCWRIVDDCGA.....QLPPKDGTPAGPSYQOYH 172

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

File: SwissProt\_37.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	704.5	77.3	171	1 IM17_RAT	O35092 rattus norv
2	703.5	77.2	171	1 IM17_HUMAN	Q99595 homo sapien
3	377.5	41.4	158	1 IM17_YEAST	P39515 saccharomyc
4	343.5	37.7	164	1 IM17_SCHPO	P87130 schizosacch
5	117	12.8	175	1 IM32_SCHPO	P87146 schizosacch
6	115.5	12.7	207	1 IM22_YEAST	O1328 saccharomyc
7	104	11.4	222	1 IM23_YEAST	P32897 saccharomyc
8	89.5	9.8	200	1 NUUM_NEUCR	P25710 neurospora
9	86	9.4	1262	1 CYA5_RAT	Q04400 rattus norv
10	83	9.1	574	1 KPYR_HUMAN	P30613 homo sapien
11	83	9.1	541	1 PTN5_MOUSE	P54830 mus musculu
12	80.5	8.8	417	1 GLYA_BORBU	O51547 borrelia bu
13	80.5	8.8	256	1 Y058_MYCTU	Q10887 mycobacteri
14	80	8.8	1123	1 DC11_DROME	P18169 drosophila
15	79	8.7	674	1 PTGA_BRELA	Q45298 brevibacter
16	78.5	8.6	1264	1 CYA5_RABIT	P40144 oryctolagus
17	77	8.5	519	1 KPYR_CANFA	Q29536 canis famil
18	76.5	8.4	347	1 TCR_STPRM	P14551 streptomyce
19	76	8.3	495	1 ACCD_MYCTU	Q10561 mycobacteri
20	75	8.2	324	1 YAGC_SCHPO	Q09875 schizosacch
21	74.5	8.2	356	1 HRPN_ERWCA	Q47279 erwinia car
22	74.5	8.2	456	1 YAJR_ECOLI	P77726 escherichia
23	73.5	8.1	466	1 HYIN_AGRRA	Q09102 agrobacteri
24	73.5	8.1	416	1 YBDA_ECOLI	P24077 escherichia
25	73	8.0	537	1 PTN5_HUMAN	P54829 homo sapien
26	73	8.0	503	1 PURR_STRLP	P42670 streptomyce
27	72.5	8.0	976	1 EP22_HUMAN	P29317 homo sapien
28	72.5	8.0	854	1 KDPP_RATRA	O34971 rathayibact
29	72.5	8.0	538	1 TCMA_STRGA	P39886 streptomyce
30	72.5	8.0	854	1 VGLB_RHGM6	P89053 rhesus cyto
31	72	7.9	247	1 SUMT_PSEFL	P37723 pseudomonas
32	71.5	7.8	574	1 KPYR_MOUSE	P53657 mus musculu
33	71.5	7.8	574	1 KPYR_RAT	P12928 rattus norv
34	71.5	7.8	288	1 M6B_MOUSE	P35803 mus musculu
35	71	7.8	750	1 ELS_CHICK	P07916 gallus gall
36	70.5	7.7	661	1 H57C_CAEEL	P27420 caenorhabdi
37	70.5	7.7	631	1 YF14_HAEIN	P40236 haemophilus
38	70	7.7	233	1 MTRD_METTM	P80183 methanobact
39	70	7.7	296	1 SAPC_ECOLI	Q47624 escherichia
40	69.5	7.6	261	1 AAC4_SALSP	P08988 salmonella
41	69.5	7.6	314	1 YM78_YEAST	Q04013 saccharomyc
42	69	7.6	324	1 PMT_YEAST	P32332 saccharomyc
43	69	7.6	284	1 TH73_MYCTU	Q59570 mycobacteri

44 69 7.6 406 1 TYRQ\_HAEIN P44747 haemophilus  
45 69 7.6 375 1 XYLH\_HAEIN P45045 haemophilus

ALIGNMENTS

RESULT 1  
IM17\_RAT  
ID IM17\_RAT STANDARD; PRT; 171 AA.  
AC O35092;  
DT 15-JUL-1998 (REL. 36, CREATED)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17 HOMOLOG.  
GN TIM17.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MORINAE; RATTUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA ISHITHARA N., MIHARA K.;  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF THE  
CC MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PUTATIVE PROTEIN-  
CC CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE (BY  
CC SIMILARITY).  
CC -!- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT  
CC LEAST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
CC INNER MEMBRANE (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE TIM17/TIM22 FAMILY.  
CC  
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CC  
CC EMBL; AB006450; D1022674; -;  
DR PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.  
KW TRANSMEM 17 37 POTENTIAL.  
FT TRANSMEM 63 83 POTENTIAL.  
FT TRANSMEM 113 133 POTENTIAL.  
SQ SEQUENCE 171 AA; 18037 MW; 6E765C35 CRC32;

Query Match 77.3%; Score 704.5; DB 1; Length 171;  
Best Local Similarity 75.4%; Pred. No. 3.4e-57;  
Matches 129; Conservative 17; Mismatches 24; Indels 1; Gaps 1;

QY 1 MEEYAREPCWRIVDDCGAFTMGVIGGVFOAIGKFRNAPVGIHRRLRGSANAVIRAP 60  
|||||  
Db 1 MEEYAREPCWRIVDDCGAFTMGVIGGVFOAIGKFRNAPVGIHRRLRGSANAVIRAP 60  
|||||  
QY 61 QIGGSFAVWGGFLFTIDCGVLRLRGKEDPNWNTSGALTGAVLAARSGPLAMVGSAMGG 120  
|||||  
Db 61 QIGGSFAVWGGFLFTIDCGVLRLRGKEDPNWNTSGALTGAVLAARSGPLAMVGSAMGG 120  
|||||  
QY 121 ILLALIEGVILLTRYTAQOFRNAPFLEDPSQLPKDCTPAGVPSYQOY 171  
|||||  
Db 121 ILLALIEGVILLTRYTAQOFRNAPFLEDPSQLPKDCTPAGVPSYQOY 171  
|||||

RESULT 2  
IM17\_HUMAN  
ID IM17\_HUMAN STANDARD; PRT; 171 AA.  
AC Q99595;  
DT 15-JUL-1998 (REL. 36, CREATED)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

Wed Aug 11 10:51:20 1999

mitochondrial inner membrane protein involved in protein import."

FEBS LETT. 349:215-221(1994).

[2] SEQUENCE FROM N.A.

RN MEDLINE; 95003211.

RA RYAN K.R., MENOLD M.M., GARRETT S., JENSEN R.E.;

RT "SMI", a high-copy suppressor of the yeast mas6 mutant, encodes an

RT essential inner membrane protein required for mitochondrial protein

RT import.;

RT MOL. BIOL. CELL 5:529-538(1994).

[3] SEQUENCE FROM N.A.

RN STRAIN=S288C / FY1679;

RC MEDLINE; 96408771.

RA KATSOULOU C., TZEREMIA M., TAVERNARAKIS N., ALEXANDRAKI D.;

RT "Sequence analysis of a 40.7 kb segment from the left arm of yeast

RT chromosome X reveals 14 known genes and 13 new open reading frames

RT including homologues of genes clustered on the right arm of

RT chromosome XI.;"

RT YEAST 12:787-797(1996).

[4] CHARACTERIZATION, AND TOPOLOGY.

RN MEDLINE; 94326924.

RA KUBERICH M., KELL P., RASOW J., DEKKER P.J.T., BLOW J., MEIJER M.;

RT "The polytopic mitochondrial inner membrane proteins MIM17 and MIM23

RT operate at the same preprotein import site.;"

RT FEBS LETT. 349:222-228(1994).

CC -1- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF

CC THE MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PUTATIVE

CC PROTEIN-CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT

CC LEAST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

CC INNER MEMBRANE.

CC -1- SIMILARITY: BELONGS TO THE TIM17/TIM22 FAMILY.

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CC EMBL; X77796; G557267; -

DR EMBL; S74018; G693752; -

DR EMBL; X87371; G854554; -

DR EMBL; Z49418; G1015553; -

DR SGD; L0001139; TIM17.

KW PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.

FT TRANSMEM 12 32 POTENTIAL.

FT TRANSMEM 59 79 POTENTIAL.

FT TRANSMEM 88 108 POTENTIAL.

FT TRANSMEM 113 133 POTENTIAL.

FT CONFLICT 33 33 H -> T (IN REF. 2).

SQ SEQUENCE 158 AA; 16584 MW; 8BDDCBFA CRC32;

Query Match 41.4%; Score 377.5; DB 1; Length 158;

Best Local Similarity 48.7%; Pred. No. 1.3e-27;

Matches 75; Conservative 26; Mismatches 50; Indels 3; Gaps 2;

QY 3 EYAREPCWRIVDCCGAFMTGIVGGVFOAIKFRNAPVGIHRLRGSANAVIRAP 62

DB 4 DHRSDPCFIVLDFGAFAMGAIGGVVHGIKFRNPLG--ERSGGAMSAIKARAPVL 61

QY 63 GGSFAVWGGLFXTIDCGILVRKGEDPNWNTSGALTGAVLAARSGPLAMVGSAMG 122

DB 62 GGNFGWGGLFTFDCAVKVRKREDPNWNTSGALTGAVLAARSGPLAMVGSAMG 121

QY 123 LALIEGVGILLTRYTAQOFR-NAPPFLEDPSPQLP 155

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17 HOMOLOG.

GN TIM17.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

[1] SEQUENCE FROM N.A.

RN BOEMER U., RASOW J., PFANNER N., MEIJER M., MAARSE A.C.;

RA SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF THE

CC MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PUTATIVE PROTEIN-

CC CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE (BY

CC SIMILARITY).

CC -1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT

CC LEAST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

CC INNER MEMBRANE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE TIM17/TIM22 FAMILY.

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CC EMBL; X97544; E243529; -

DR PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.

KW TRANSMEM 17 37 POTENTIAL.

FT TRANSMEM 63 83 POTENTIAL.

FT TRANSMEM 113 133 POTENTIAL.

SQ SEQUENCE 171 AA; 18023 MW; 6408G99C CRC32;

Query Match 77.2%; Score 703.5; DB 1; Length 171;

Best Local Similarity 75.4%; Pred. No. 4.2e-57;

Matches 129; Conservative 17; Mismatches 24; Indels 1; Gaps 1;

QY 1 MEYAREPCWRIVDCCGAFMTGIVGGVFOAIKFRNAPVGIHRLRGSANAVIRAP 60

DB 1 MEYAREPCWRIVDCCGAFMTGIVGGVFOAIKFRNAPVGIHRLRGSANAVIRAP 60

QY 61 QIGGSFAVWGGLFXTIDCGILVRKGEDPNWNTSGALTGAVLAARSGPLAMVGSAMG 120

DB 61 QIGGSFAVWGGLFXTIDCGILVRKGEDPNWNTSGALTGAVLAARSGPLAMVGSAMG 120

QY 121 LALIEGVGILLTRYTAQOFRNAPPFLEDPSPQLPKDGTAPGYPYQOY 171

DB 121 LALIEGVGILLTRYTAQOFRNAPPFLEDPSPQLPKDGTAPGYPYQOY 170

RESULT 3

ID IM17\_YEAST STANDARD; PRT; 158 AA.

AC P39515; Q02310.

DT 01-FEB-1995 (REL. 31, CREATED)

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17

DE (MITOCHONDRIAL PROTEIN IMPORT PROTEIN 2) (MITOCHONDRIAL INNER MEMBRANE

DE PROTEIN MIM17).

GN TIM17 OR MIM17 OR MIM17 OR MIM17 OR YJL143W OR J0648.

OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCHAROMYCETALES;

OC SACCHAROMYCETACEAE; SACCHAROMYCES.

CC [1]

RN SEQUENCE FROM N.A.

RC STRAIN=ATCC 77162;

RX MEDLINE; 94326923.

RA MAARSE A.C., BLOW J., KELL P., PFANNER N., MEIJER M.;

RT "Identification of the essential yeast protein MIM17, an integral



RT	mitochondrial protein import pathway.*;
RL	J. CELL BIOL. 122:1003-1012(1993).
RN	{2}
RN	SEQUENCE FROM N.A.
RP	
RP	MEDLINE: 93380573.
PY	

DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE NADH-UBIQUINONE OXIDOREDUCTASE 21.3 KD SUBUNIT (EC 1.6.5.3)  
 DE (EC 1.6.99.3).  
 OS NEUROSPORA CRASSA.  
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;  
 OC SORDARIALES; SORDARIACEAE; NEUROSPORA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ST. LAWRENCE 74 / SL 74 / ORS 6A;  
 RX MEDLINE; 91159490.  
 RA NEHLS U., HEMMER S., ROEHLER D.A., VAN DER PAS J.C., PREIS D.,  
 RA SACKMANN U., WEISS H.,  
 RT "cDNA and genomic DNA sequence of the 21.3 kDa subunit of  
 RT NADH:ubiquinone reductase (complex I) from Neurospora crassa.";  
 RL BIOCHIM. BIOPHYS. ACTA 1088:325-326(1991).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE.  
 CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.  
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -----  
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 CC -----  
 CC EMBL; X56612; G3050; -  
 DR PIR; S14277; S14277.  
 KW OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.  
 SQ SEQUENCE 200 AA; 21349 MW; A0B12273 CRC32;  
 -----  
 Query Match 9.8%; Score 89.5; DB 1; Length 200;  
 Best Local Similarity 27.1%; Pred. No. 0.19;  
 Matches 32; Conservative 14; Mismatches 57; Indels 15; Gaps 3;  
 QY 63 GG---SFAVWGGLFXTIDCGLVRLRKEPDWNSITSGALTGAVALAARS--GPLAMVGSAM 117  
 DB 55 GGTIIISFTLAGGIYRQAQASANLREKEDGNHAIAGFLGSGVMGLSLRFPVILFGAM 114  
 QY 118 MCGILLALIEGVIL-----LTRYTAQOFNAPPELDPDPSQLPKDGTAPAGY 165  
 D 115 AGSVGAFASFGLTGWGRDPNVDFERKEAMRLNRRRVPVEETLAEVGEGRGIYPFGY 172  
 -----  
 RESULT 9  
 CYA5\_RAT  
 ID CYA5\_RAT STANDARD; PRT; 1262 AA.  
 AC Q04400;  
 DT 01-OCT-1993 (REL. 27, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)  
 DE (ADENYLATE CYCLASE).  
 GN ADCY5.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, KIDNEY, AND HEART;  
 RA PREMONT R.T.;  
 RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE OF 164-1262 FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE; 93028552.

RA PREMONT R.T., CHEN J., MA H.-W., PONNAPALLI M., IYENGAR R.;  
 RT "Two members of a widely expressed subfamily of hormone-stimulated  
 RT adenylyl cyclases.";  
 RL PROC. NATL. ACAD. SCI. U.S.A. 89:9809-9813(1992).  
 CC -!- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-INSENSITIVE ADENYLIL  
 CC CYCLASE.  
 CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.  
 CC -!- ENZYME REGULATION: INSENSITIVE TO CA(2+)/CALMODULIN. STIMULATED BY  
 CC THE G PROTEIN BETA & GAMMA SUBUNIT COMPLEX.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS TWO  
 CC DOMAINS WITH 6 POTENTIAL TRANSMEMBRANE REGIONS EACH.  
 CC -!- SIMILARITY: THE TWO CYTOPLASMIC DOMAINS ARE SIMILAR TO ONE  
 CC ANOTHER AND TO THE CATALYTIC DOMAINS OF GUANYLATE CYCLASES.  
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 CC -----  
 CC EMBL; M96159; G1758332; -  
 DR PROSITE; P500452; GUANYLATE\_CYCLASES; 2.  
 DR PFAM; PF00211; guanylate\_cyc; 2.  
 DR HSP; P19754; LANK.  
 KW LYASE; CAMP SYNTHESIS; TRANSMEMBRANE; GLYCOPROTEIN; DUPLICATION.  
 FT DOMAIN 1 242 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 243 263 POTENTIAL.  
 FT TRANSMEM 269 289 POTENTIAL.  
 FT TRANSMEM 300 320 POTENTIAL.  
 FT TRANSMEM 326 346 POTENTIAL.  
 FT TRANSMEM 351 371 POTENTIAL.  
 FT TRANSMEM 375 395 POTENTIAL.  
 FT DOMAIN 396 763 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 764 784 POTENTIAL.  
 FT TRANSMEM 790 810 POTENTIAL.  
 FT TRANSMEM 837 857 POTENTIAL.  
 FT DOMAIN 858 910 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 911 931 POTENTIAL.  
 FT TRANSMEM 936 956 POTENTIAL.  
 FT TRANSMEM 985 1005 POTENTIAL.  
 FT DOMAIN 1006 1262 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 1262 AA; 139178 MW; 3F17897B CRC32;  
 -----  
 Query Match 9.4%; Score 86; DB 1; Length 1262;  
 Best Local Similarity 26.2%; Pred. No. 2.7;  
 Matches 42; Conservative 15; Mismatches 43; Indels 60; Gaps 7;  
 QY 11 WRIVDDCGGAFITMG---VIGGGVFQAIKGRNAPV-----GIRHLRGSANAVR 56  
 DB 73 WRGGDDDEDPPLSGDDPLVGGFGF-----SFRKSAMQERGGDDGGRRQRRAAGGS 128  
 QY 57 IRAPQIGGS-----FAVWGGFLF---XTIDCGLVRLRGRK-----E 87  
 DB 129 TRAPPAGGSGSSSAAAAAGGTEVPRSVGVLEERGRGAAEELEPGTGTVEDGDGSE 188  
 QY 88 DPWNSTSGALTGAVALAARSGLPLAMVGSAMGGLIALIE 127  
 DB 189 DGGSSVAGSGTGTLS-----LGACCLALLQ 215  
 -----  
 RESULT 10  
 KPYR\_HUMAN  
 ID KPYR\_HUMAN STANDARD; PRT; 574 AA.  
 AC P30613; P11973;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
 DE PYRUVATE KINASE, ISOZYMES R/L (EC 2.7.1.40).  
 GN PKLR OR PKL OR PKL.  
 OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
 RN [1]  
 RN SEQUENCE FROM N.A., AND VARIANT TOKYO.  
 RX MEDLINE; 91376115.  
 RX KANNO H., FUJII H., HIRONO A., MIWA S.;  
 RA "CDNA cloning of human R-type pyruvate kinase and identification of a  
 RT single amino acid substitution (Thr384->Met) affecting enzymatic  
 RT stability in a pyruvate kinase variant (PK Tokyo) associated with  
 RT hereditary hemolytic anemia";  
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:8218-8221(1991).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 88158079.  
 RX TAN K., FUJII H., NAGATA S., MIWA S.;  
 RA "Human liver type pyruvate kinase: complete amino acid sequence and  
 RT the expression in mammalian cells";  
 RL PROC. NATL. ACAD. SCI. U.S.A. 85:1792-1795(1988).  
 RN [3]  
 RN SEQUENCE OF 470-574 FROM N.A.  
 RP MEDLINE; 87184521.  
 RX TAN K., FUJII H., TSUTSUMI H., SUKEGAWA J., TOYOSHIMA K.,  
 RA YOSHIDA M.C., NOGUCHI T., TANAKA T., MIWA S.;  
 RT "Human liver type pyruvate kinase: cDNA cloning and chromosomal  
 RT assignment";  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 143:431-438(1987).  
 RN [4]  
 RN VARIANTS LINZ AND BEIRUT.  
 RP MEDLINE; 91208396.  
 RX NEUBAUER B., LAKOMEK M., WINKLER H., PARKE M., HOFFERBERT S.,  
 RA SCHROTER W.;  
 RT "Point mutations in the L-type pyruvate kinase gene of two children  
 RT with hemolytic anemia caused by pyruvate kinase deficiency";  
 RL BLOOD 77:1871-1875(1991).  
 RN [5]  
 RN VARIANT FUKUSHIMA/MAEBASHI.  
 RP MEDLINE; 92163106.  
 RX KANNO H., FUJII H., HIRONO A., OMINE M., MIWA S.;  
 RA "Identical point mutations of the R-type pyruvate kinase (PK) cDNA  
 RT found in unrelated PK variants associated with hereditary hemolytic  
 RT anemia";  
 RL BLOOD 79:1347-1350(1992).  
 RN [6]  
 RN SEQUENCE OF 365-431 FROM N.A., AND VARIANT OSAKA.  
 RP MEDLINE; 92326593.  
 RX KANNO H., FUJII H., TSUJINO G., MIWA S.;  
 RA "Molecular basis of impaired pyruvate kinase isozyme conversion in  
 RT erythroid cells: a single amino acid substitution near the active  
 RT site and decreased mRNA content of the R-type PK";  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 192:46-52(1993).  
 RN [7]  
 RN REVIEW ON VARIANTS.  
 RP MEDLINE; 96263732.  
 RX BEUTLER E., BARONCIANI L.;  
 RA "Mutations in pyruvate kinase";  
 RL HUM. MUTAT. 7:1-6(1995).  
 RN [8]  
 RN VARIANTS SAPPORO GLN-426.  
 RP MEDLINE; 93244440.  
 RX KANNO H., FUJII H., MIWA S.;  
 RA "Low substrate affinity of pyruvate kinase variant (PK Sapporo)  
 RT caused by a single amino acid substitution (426 Arg->Gln) associated  
 RT with hereditary hemolytic anemia";  
 RL BLOOD 81:2439-2441(1993).  
 RN [9]  
 RN VARIANTS D-134; P-155; H-359; W-486; V-495 AND Q-510.  
 RP MEDLINE; 93248282.  
 RX BARONCIANI L., BEUTLER E.;  
 RA "Analysis of pyruvate kinase-deficiency mutations that produce  
 RT nonspherocytic hemolytic anemia";  
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:4324-4327(1993).  
 RN [10]  
 RN VARIANTS S-332; S-336; K-354 DEL; D-361; T-392; H-498; Q-510 & W-532.  
 RP MEDLINE; 94235845.  
 RX LENZNER C., NUERNBERG P., THIELE B.-J., REIS A., BRABEC V.,  
 RA SAKALOVA A., JACOBASCH G.;  
 RT "Mutations in the pyruvate kinase L gene in patients with hereditary  
 RT hemolytic anemia";  
 RL BLOOD 83:2817-2822(1994).  
 RN [11]  
 RN VARIANTS E-331; A-341; K-393; S-393; D-458; M-460 AND H-498.  
 RP MEDLINE; 95221622.  
 RX BARONCIANI L., BEUTLER E.;  
 RA "Molecular study of pyruvate kinase deficient patients with  
 RT hereditary nonspherocytic hemolytic anemia";  
 RL J. CLIN. INVEST. 95:1702-1709(1995).  
 RN [12]  
 RN VARIANTS HNSHA.  
 RP BARONCIANI L., WESTWOOD B., BEUTLER E.;  
 RA "Study of the molecular defects in pyruvate kinase (PK) deficient  
 RT patients affected by hereditary nonspherocytic hemolytic anemia  
 RT (HNSHA)";  
 RL J. INVEST. MED. 43:341A-341A(1995).  
 RN [13]  
 RN VARIANTS Q-172; Q-337; Q-339; T-357; I-408; T-431; W-486 & Q-532.  
 RX MEDLINE; 99043610.  
 RA ZARZA R., ALVAREZ R., PUJADES A., NOMDEU B., CARRERA A., ESTELLA J.,  
 RA REMACHA A., SANCHEZ J.M., MOREY M., CORTES T., PEREZ LUNGUS G.,  
 RA BUREO E., VIVES CORRONS J.L.;  
 RT "Molecular characterization of the PK-LR gene in pyruvate kinase  
 RT deficient Spanish patients";  
 RL BR. J. HAEMATOL. 103:377-382(1998).  
 RN [14]  
 RN VARIANTS HNSHA S-332; P-337; W-486; C-498 AND Q-510.  
 RP MEDLINE; 98141680.  
 RX PASTORE L., DELLA MORTE R., FRISIO G., ALFINITO F., VITALE D.,  
 RA CALISE R.M., FERRARO F., ZAGARI A., ROTOLI B., SALVATORE F.;  
 RT "Novel mutations and structural implications in R-type pyruvate  
 RT kinase-deficient patients from Southern Italy";  
 RL HUM. MUTAT. 11:127-134(1998).  
 CC -1- CATALYTIC ACTIVITY: ATP + PYRUVATE = ADP + PHOSPHOENOLPYRUVATE.  
 CC -1- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.  
 CC -1- PATHWAY: FINAL STEP IN GLYCOLYSIS.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
 CC -1- DISEASE: DEFECTS IN PYRUVATE KINASE ARE THE MOST COMMON CAUSES  
 CC FOR HEREDITARY NONSPHEROCYTIC HEMOLYTIC ANEMIA (HNSHA) AMONG  
 CC GLYCOLYTIC ENZYMES.  
 CC -1- THERE ARE 4 ISOZYMES OF PYRUVATE KINASE IN MAMMALS: L, R, M1 AND  
 CC M2. L TYPE IS MAJOR ISOZYME IN THE LIVER. R IS FOUND IN RED  
 CC CELLS, M1 IS THE MAIN FORM IN MUSCLE, HEART AND BRAIN, AND M2 IS  
 CC FOUND IN EARLY FETAL TISSUES.  
 CC -1- ALTERNATIVE PRODUCTS: THE L- AND R-TYPE ISOZYMES ARE PRODUCED  
 CC FROM A SINGLE GENE BY USE OF DIFFERENT PROMOTERS. THE SEQUENCE  
 CC SHOWN HERE IS THAT OF THE R-TYPE.  
 CC -1- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D10326; G220036; -.  
 CC EMBL; M15465; G189996; -.  
 CC EMBL; S60712; G299641; -.  
 CC PIR; A30150; A30150.  
 CC PIR; A29414; A29414.  
 CC SWISS-2DPAGE; P30613; HUMAN.  
 CC MIN; 266200; -.  
 CC PROSITE; PS00110; PYRUVATE\_KINASE; 1.  
 CC PFAM; PF00224; PK; 1.  
 CC HSP; P11974; 1PK.  
 KW TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY; PHOSPHORYLATION;  
 KW MAGNESIUM; ALTERNATIVE SPLICING; DISEASE MUTATION.

```
FT MOD_RES 43 43 PHOSPHORYLATION (BY CAPK).
FT ACT_SITE 313 313 BY SIMILARITY.
FT METAL 315 315 MAGNESIUM (POTENTIAL).
FT METAL 336 336 MAGNESIUM (POTENTIAL).
FT METAL 337 337 MAGNESIUM (POTENTIAL).
FT VARSPLIC 1 33 MTSOENISSQLRSWYSQSDRLAKSILIGAPG -> ME
FT VARIANT 107 107 M -> T (IN HEMOLYTIC ANEMIA).
FT VARIANT 131 131 MISSING (IN HEMOLYTIC ANEMIA).
FT VARIANT 134 134 V -> D (IN HEMOLYTIC ANEMIA).
FT VARIANT 155 155 L -> P (IN HEMOLYTIC ANEMIA).
FT VARIANT 172 172 E -> Q (IN HEMOLYTIC ANEMIA).
FT VARIANT 163 163 R -> C (IN HEMOLYTIC ANEMIA).
FT VARIANT 221 221 D -> DD (IN HEMOLYTIC ANEMIA; LINZ).
FT VARIANT 275 275 G -> R (IN HEMOLYTIC ANEMIA).
FT VARIANT 281 281 D -> N (IN HEMOLYTIC ANEMIA).
FT VARIANT 287 287 F -> V (IN HEMOLYTIC ANEMIA).
FT VARIANT 314 314 I -> T (IN HEMOLYTIC ANEMIA).
FT VARIANT 331 331 D -> E (IN HEMOLYTIC ANEMIA).
FT VARIANT 332 332 G -> S (IN HEMOLYTIC ANEMIA).
FT VARIANT 336 336 A -> S (IN HEMOLYTIC ANEMIA).
FT VARIANT 337 337 R -> P (IN HEMOLYTIC ANEMIA).
FT VARIANT 337 337 R -> Q (IN HEMOLYTIC ANEMIA).
FT VARIANT 339 339 D -> Q (IN HEMOLYTIC ANEMIA).
FT VARIANT 341 341 G -> A (IN HEMOLYTIC ANEMIA).
FT VARIANT 354 354 MISSING (IN HEMOLYTIC ANEMIA).
FT VARIANT 357 357 I -> T (IN HEMOLYTIC ANEMIA).
FT VARIANT 359 359 R -> C (IN HEMOLYTIC ANEMIA).
FT VARIANT 359 359 R -> H (IN HEMOLYTIC ANEMIA).
FT VARIANT 361 361 N -> D (IN HEMOLYTIC ANEMIA).
FT VARIANT 368 368 V -> F (IN HEMOLYTIC ANEMIA; OSAKA).
FT VARIANT 384 384 T -> M (IN HEMOLYTIC ANEMIA; TOKYO/
FT BEIRUT; MOST COMMON MUTATION IN JAPANESE
FT POPULATION).
FT VARIANT 392 392 A -> T (IN HEMOLYTIC ANEMIA).
FT VARIANT 393 393 N -> K (IN HEMOLYTIC ANEMIA).
FT VARIANT 393 393 N -> S (IN HEMOLYTIC ANEMIA).
FT VARIANT 401 401 C -> CS (IN HEMOLYTIC ANEMIA).
FT VARIANT 408 408 T -> I (IN HEMOLYTIC ANEMIA).
FT VARIANT 421 421 Q -> K (IN HEMOLYTIC ANEMIA; FUKUSHIMA/
FT MAEBASHI).
FT VARIANT 426 426 R -> Q (IN HEMOLYTIC ANEMIA; SAPPORO).
FT VARIANT 426 426 R -> W (IN HEMOLYTIC ANEMIA).
FT VARIANT 431 431 A -> T (IN HEMOLYTIC ANEMIA).
FT VARIANT 458 458 G -> D (IN HEMOLYTIC ANEMIA).
FT VARIANT 459 459 A -> V (IN HEMOLYTIC ANEMIA).
FT Query Match 9.1%; Score 83; DB 1; Length 574;
FT Local Similarity 26.7%; Pred. No. 2.2;
FT Matches 31; Conservative 20; Mismatches 55; Indels 10; Gaps 3;
QY 1 MEYAREPCWRIV---DCGGAFTMGVGGVFOAIGFRNAPVGI---RHRLRGS 52
DB 138 VESFAGSPLSYRPVATALDTKGEIRTGILGGPESEVELVKSQVLVTVDPAFRTRG 197
QY 53 NAVRIRAPQIGGSFAVWGGLFTXIDCGLVRLRGKEDPWNISITGALTGAVIAARS 108
DB 198 NTWVDYDYNVRVVPVGGRIY--IDDLISLVVQKISPEGLVTQVENGVLGSRKG 251
RESULT 11
ID PTN5_MOUSE STANDARD; PRT; 541 AA.
AC P54830; Q64694;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP)
DE (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE).
GN PTPN5
OS 'MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE; 96115113.
RA SHARMA E., ZHAO F., BULT A., LOMBROSO P.J.;
RT "Identification of two alternatively spliced transcripts of STEP: a
subfamily of brain-enriched protein tyrosine phosphatases.";
RL BRAIN RES. MOL. BRAIN RES. 32:87-93(1995).
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -!- TISSUE SPECIFICITY: STEP20 IS EXPRESSED ONLY IN THE CNS.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS ARE PRODUCED BY
ALTERNATIVE SPLICING: STEP61 (SHOWN HERE), STEP46, STEP38 AND
STEP20. STEP38 AND STEP20 LACK THE CATALYTIC DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U28217; G915382; -.
DR EMBL; U28216; G915380; -.
DR EMBL; S80329; G1245880; -.
DR MGD; MGI:97807; PTPN5.
DR PROSITE; P500383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; P500056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; P500055; TYR_PHOSPHATASE_PTP; 1.
DR PFAM; PF00102; Y_phosphatase; 1.
DR HSP; P18052; 1YFO.
KW HYDROLASE; ALTERNATIVE SPLICING.
FT DOMAIN 290 533 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 472 472 BY SIMILARITY.
FT VARSPLIC 1 173 MISSING (IN STEP20 AND STEP46).
FT VARSPLIC 337 346 GYSGEKVYI -> VCSISIPRAH (IN STEP38 AND
STEP20).
FT VARSPLIC 347 541 MISSING (IN STEP38 AND STEP20).
FT SEQUENCE 541 AA; 60829 MW; 9C9F4460 CRC32;
Query Match 9.1%; Score 83; DB 1; Length 541;
Best Local Similarity 28.9%; Pred. No. 2.1;
Matches 24; Conservative 15; Mismatches 40; Indels 4; Gaps 3;
QY 78 CGLVRLRGKEDPWNISITGALTGAVIAARS-GPLAMVGSAMMGILLALIE-GVGILLTR 135
DB 76 CGVLWLSGHHGHWLQNTDLSISLTVLNHLGVPVAMLGSGTGWGIPSLLLVSLVIVT 135
QY 136 YTAQQRNAPPFLEDPQLPKD 158
DB 136 TLVWHLKAPP--EPPAPLPED 156
RESULT 12
GLYA_BORBU STANDARD; PRT; 417 AA.
ID GLYA_BORBU
AC O51547;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.1.2.1) (SERINE METHYLASE)
DE (SHMT).
GN GLYA OR BB0601.
OS BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; BORRELIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35210 / B31;
RX MEDLINE; 98065943.
```



FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,  
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,  
DOUGHERTY B., TOMB J.-F., FLETSCHMANN R.D., RICHARDSON D.,  
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,  
VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,  
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,  
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,  
SMITH H.O., VENTER J.C.;  
"Genomic sequence of a Lyme disease spirochaete, Borrelia  
burgdorferi".  
NATURE 350:580-586(1997).  
-|- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.  
-|- CATALYTIC ACTIVITY: 5,10-METHYLENETETRAHYDROFOLATE + GLYCINE +  
H(2)O = TETRAHYDROFOLATE + L-SERINE.  
-|- COFACTOR: PYRIDOXAL PHOSPHATE.  
-|- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS,  
HORMONES AND OTHER COMPONENTS.  
-|- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
-|- SUBCELLULAR LOCATION: CYTOPLASMIC.  
-|- SIMILARITY: BELONGS TO THE SHMT FAMILY.  
-----  
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-----  
EMBL; AE001161; G2688518; -  
TIGR; B06001; -  
PROSITE; PS00096; SHMT; 1.  
TRANSFERASE; PYRIDOXAL PHOSPHATE; ONE-CARBON METABOLISM.  
BINDING 221 221 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SEQUENCE 417 AA; 45881 MW; D070203A CRC32;  
-----  
Query Match 8.8%; Score 80.5; DB 1; Length 417;  
Best Local Similarity 26.4%; Pred. No. 2.6;  
Matches 38; Conservative 16; Mismatches 61; Indels 29; Gaps 8;  
  
QY 13 IVDD-----CGGFTMGVIGGGVFOAIKGFNRNAPVIGVIRHRLRGSANAVIRAPQIGGSF 66  
DB 181 TADVSAYLLCDIAHAGLI-----VAGFNSSIDVAH-LTTSTHTKLRGP--GGI 230  
  
QY 67 AVWGGLFTYIDGVLVRLRGKEDP-WNSITGALTGAVLAARSGPLAMVGSAMNGTILLAL 125  
DB 231 ILSGKDFDK----LVNFNGKEKPLFNNAVNSTVFP-----TQGGPLVHV-----TAGRAIAF 278  
  
126 IEGVGILLTRYTAQOFRNAPPFLE 149  
DB 279 KEALQESFEKIYANIKTKVNAE 302  
  
RESULT 13  
Y058-MYCTU  
ID Y058-MYCTU STANDARD; PRT; 256 AA.  
AC Q10887;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL 27.8 KD PROTEIN CY251.08.  
GN MTCV251.08  
OS MYCOBACTERIUM TUBERCULOSIS  
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;  
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-H37RV;  
RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;  
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
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SQ SEQUENCE 1123 AA; 127959 MW; 99218239 CRC32;

Query Match      8.8%; Score 80; DB 1; Length 1123;
Best Local Similarity 24.7%; Pred. No. 8.3;
Matches 44; Conservative 16; Mismatches 66; Indels 52; Gaps 10;

QY 24 GVIGGVQFAIKGFNAPVGI-----RRLRGSANAVRIRA-----PQIGGS 65
DB 952 GVGGSQ--KSNPNPTTLTPAQEQPQEHVHKSPSSAPSETEIENAPSSDPQVGS 1009
QY 66 FAVWGGLFXTDCGLVRLRGKEDPWN-----ITSGALTGAVALAARSG----PLAM 112
DB 1010 FYTGSELLHPF-WGLLPVERPDPNKPYPDPHPLYTGGGSYDAYL--RDRGHRDTHI 1066
QY 113 VGSAMWGGILLALIDGVGL--LTRYTAQQRNAPFFLEDPSLPKDGTPAGPSPSY 168
DB 1067 MQGQTGHGILTP-----GMLERLLRIKMDQRRFPFIQGYAESP-----YESY 1110

R 15
PTGA_BRELA
AC Q45298;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (GLUCOSE-
DE PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
DE COMPONENT) (EC 2.7.1.69) (EII-GLC / EIII-GLC).
GN PTSG.
OS BREVI BACTERIUM LACTO FERMENTUM.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIADAE;
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; CORYNEBACTERIACEAE;
OC CORYNEBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13869;
RA YOON K.H.;
RL SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
CC -TRANSPORT SYSTEM. THE IID DOMAINS CONTAIN THE SUGAR BINDING SITE
CC AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
CC THE SUGAR.
CC -!- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
CC PROTEIN HISTIDINE + SUGAR PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
CC -!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
CC -!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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CC -----
DR EMBL; L18875; G405143;
DR PROSITE; PS00371; PTS_EIIA_1; 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
DR PFAM; PF00358; PTS_EIIA_1; 1.
DR PFAM; PF00367; PTS_EIIB; 1.
DR HSP; P08837; 2F3G.
KW PHOSPHOTRANSFERASE SYSTEM; SUGAR TRANSPORT; TRANSFERASE;
FT 'DOMAIN 1 ? EIIB DOMAIN.
FT 'DOMAIN ? ? EIIC DOMAIN.
FT 'DOMAIN ? 674 EIIA DOMAIN.
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FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 162 182 POTENTIAL.
FT TRANSMEM 193 213 POTENTIAL.
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 303 323 POTENTIAL.
FT TRANSMEM 344 364 POTENTIAL.
FT TRANSMEM 377 397 POTENTIAL.
FT TRANSMEM 409 429 POTENTIAL.
FT TRANSMEM 442 462 POTENTIAL.
FT TRANSMEM 493 513 POTENTIAL.
FT MOD_RES 28 28 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 594 594 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 674 AA; 71626 MW; C21F0F14 CRC32;

Query Match      8.7%; Score 79; DB 1; Length 674;
Best Local Similarity 23.2%; Pred. No. 6;
Matches 35; Conservative 19; Mismatches 51; Indels 46; Gaps 7;

QY 19 GAFTMGVIGGVQFAIKGFN-----APVGIHRLRGSANAVRIR-AP 60
DB 280 GPFGIGV-GNGISSLEAVNNFSPFILSIVIPLLYPFLVPLGLHWPL-----NAIMIQNLN 334
QY 61 QIGGSFAVWGGFLXTIDCGLVRLRGKEDPWNISITSGALTGAVALAARSGPLAMVGSAMMGG 120
DB 335 TLGYDF-----IQPGMAWNAFACFLVTGVFLIALKEKKNRAMQVSLGG 378
QY 121 ILLALIEGV-----GILLTRYTAQQRNAP 145
DB 379 MLAGLGGISEPSLYGVLL-RFKKTYFRLLP 408
```

Search completed: August 10, 1999, 08:35:42  
Job time: 8499 sec

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RESULT 4  
US-08-804-227C-11  
Sequence 11, Application US/08804227C  
Patent No. 5876991  
GENERAL INFORMATION:  
APPLICANT: Dehoff, Bradley S.  
APPLICANT: Kuhstoss, Stuart A.  
APPLICANT: Rostock, Paul R., Jr.  
APPLICANT: Sutton, Kimberly L.  
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: THOMAS G. PLANT 1501  
STREET: LILLY CORPORATE CENTER  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII(DOS) Text only  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,227C  
FILING DATE: February 21, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Plant, Thomas G.  
REGISTRATION NUMBER: 35,784  
REFERENCE/DOCKET NUMBER: X-8231  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-276-2459  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1580 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-804-227C-11

Query Match 8.6%; Score 78; DB 2; Length 1580;  
Best Local Similarity 27.7%; Pred. No. 2.2;  
Matches 39; Conservative 18; Mismatches 50; Indels 34; Gaps 7;  
QY 11 WRIVDC---GGAFTMGVIGGGVFOAIKRGFRNAPVGIHRRLRGSANAVIRAPQIGGSA 67  
DB 1107 WRVAVVAVAGGEGEDQVAVRGGGVF---GRLVGVGV---RGGSGVWRAR---GCVV 1153  
QY 68 WGGGLFTXIIDCGLVRLRKGKEDPWNISITSGALTGAVLAARSGPLAVG-----115  
DB 1154 VTGGL-GGVGGHVAHWLARSAGAEHVVLACGRGGGVVGAVALERELVGLGAKVTFVSCDVG 1212  
QY 115 ---SAMMGGILTLALIEGVGILT 133  
DB 1213 DRASWG--LLGVVEGGLVPL 1231

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[illegible]

Db 121 ILLALIEGVILLTRYTAQFRNAPPPLEDSQLPKDGTGTPAGYPSYQYH 172  
|||||

## RESULT 2

US-08-812-645-3

; Sequence 3, Application US/08812645

; Patent No. 5854414

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Suriya K.

; TITLE OF INVENTION: NOVEL HUMAN MITOCHONDRIAL

; TITLE OF INVENTION: MEMBRANE PROTEIN

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/812,645

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: To Be Assigned

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0229 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 171 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; LIBRARY: Genbank

; CLONE: GI 1770564

US-08-812-645-3

Query Match 77.2%; Score 703.5; DB 2; Length 171;  
Best Local Similarity 75.4%; Pred. No. 6.1e-74;  
Matches 129; Conservative 17; Mismatches 24; Indels 1; Gaps 1;

QY 1 MEEYAREPCWRIVDGCGAFTMGVIGGVFOAIKGFERNAPVGIHRHLSANAVIRAP 60  
|||||  
Db 1 MEEYAREPCWRIVDGCGAFTMGVIGGVFOAIKGFERNAPVGIHRHLSANAVIRAP 60  
|||||  
QY 61 QIGGSFVWVGGLFXTIDCGLVRLRKEDPNWNSITSGALTGAVALAARSGPLAMVGSAMMG 120  
|||||  
Db 61 QIGGSFVWVGGLFXTIDCGLVRLRKEDPNWNSITSGALTGAVALAARSGPLAMVGSAMMG 120  
|||||  
QY 121 ILLALIEGVILLTRYTAQFRNAPPPLEDSQLPKDGTGTPAGYPSYQY 171  
|||||  
Db 121 ILLALIEGVILLTRYTAQFRNAPPPLEDSQLPKDGTGTPAGYPSYQY 170  
|||||

## RESULT 3

US-08-812-645-4

; Sequence 4, Application US/08812645

; Patent No. 5854414  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Goli, Suriya K.  
; TITLE OF INVENTION: NOVEL HUMAN MITOCHONDRIAL  
; TITLE OF INVENTION: MEMBRANE PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/812,645  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: To Be Assigned  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0229 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 158 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; LIBRARY: Genbank  
; CLONE: GI 557267  
; US-08-812-645-4

Query Match 41.4%; Score 377.5; DB 2; Length 158;  
Best Local Similarity 48.7%; Pred. No. 2.4e-36;  
Matches 75; Conservative 26; Mismatches 50; Indels 3; Gaps 2;

QY 3 EYAREPCWRIVDGCGAFTMGVIGGVFOAIKGFERNAPVGIHRHLSANAVIRAPQI 62  
|||||  
Db 4 DHSRDCPIVLNDFGAFAMGAIGGVVHGIKGFNSPLG--ERSGAMSAIKARAPVL 61  
|||||  
QY 63 GGSFVWVGGLFXTIDCGLVRLRKEDPNWNSITSGALTGAVALAARSGPLAMVGSAMMG 122  
|||||  
Db 62 GGNFVWVGGLFXTIDCGLVRLRKEDPNWNSITSGALTGAVALAARSGPLAMVGSAMMG 121  
|||||  
QY 123 LALIEGVILLTRYTAQFRNAPPPLEDSQLP 155  
|||||  
Db 122 LGVIEGVGLMFQRYAAQAKPMAPLPPEAPSSQP 155  
|||||

## RESULT 4

US-08-804-227C-11

; Sequence 11, Application US/08804227C

; Patent No. 5876991

; GENERAL INFORMATION:

; APPLICANT: DeHoff, Bradley S.

; APPLICANT: Kuhstoss, Stuart A.

; APPLICANT: Rostock, Paul R., Jr.

; APPLICANT: Sutton, Kimberly L.

; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES





Best Local Similarity 27.0%; Pred. No. 3.7;  
Matches 34; Conservative 19; Mismatches 48; Indels 25; Gaps 6;  
QY 24 GVIGGVFQAICGF-RNAPVGIHRL-----RGSANAVR-----IRAPQIGSFVAV--- 69  
DB 602 GVPGLGVGAGVPGFAGAGDEGVRRSLSPELREGDPFSSQHLPTSPSSPRVPGALAAKAA 661  
QY 69 -WGGLEFXTIDCGVLRKREDPWNISITG---ALTGAVLAARSGLAMVGSMMGGILLA 124  
DB 662 KYGAAPVGLGGLGALGGVIGFEGVVGAGPAAAKAAAKAAQFGLVGAAGLGL--- 719  
QY 125 LIEGVG 130  
DB 719 ---GVG 721

RESULT 8  
PCT-US95-04681-18  
; Sequence 18, Application PC/TUS9504681  
; GENERAL INFORMATION:  
; APPLICANT: FOX, Gary M.  
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04681  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 976 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-04681-18

Query Match 8.0%; Score 72.5; DB 3; Length 976;  
Best Local Similarity 23.6%; Pred. No. 4.9;  
Matches 29; Conservative 22; Mismatches 53; Indels 19; Gaps 5;  
QY 44 IRHRLGSANAVRIRAPQIGGSFAVWGGFLXTID-----CGLVLRKREDPWNISITGA 97  
DB 471 VTYRKGDNSYNVRTE-----GFSVTLDDLAPDTTILVQVQALTEQGAGSKV 521  
QY 98 LTGAVLAAR-SGFLAMVGSMMGGILLALIEGVGILL-TRYTAQQRNAPP--ELEDPSQ 153  
DB 522 HEFOTLSPGSGNLAVIGGVAVGVLLVLAVGVFFIHRRRKNQRARQSPEDVYFSKSEQ 581  
QY 154 LPP 156  
DB 582 LKP 584  
RESULT 9  
US-08-804-227C-4  
; Sequence 4, Application US/08804227C

TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 977  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
US-08-673-789-8

Query Match 8.0%; Score 72.5; DB 2; Length 977;  
Best Local Similarity 23.6%; Pred. No. 4.9;  
Matches 29; Conservative 22; Mismatches 53; Indels 19; Gaps 5;  
QY 44 IRHRLGSANAVRIRAPQIGGSFAVWGGFLXTID-----CGLVLRKREDPWNISITGA 97  
DB 472 VTYRKGDNSYNVRTE-----GFSVTLDDLAPDTTILVQVQALTEQGAGSKV 522  
QY 98 LTGAVLAAR-SGFLAMVGSMMGGILLALIEGVGILL-TRYTAQQRNAPP--ELEDPSQ 153  
DB 523 HEFOTLSPGSGNLAVIGGVAVGVLLVLAVGVFFIHRRRKNQRARQSPEDVYFSKSEQ 582  
QY 154 LPP 156  
DB 583 LKP 585

RESULT 7  
US-08-678-039A-40  
; Sequence 40, Application US/08678039A  
; Patent No. 5858662  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Morris, Colleen A.  
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and  
; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the  
; TITLE OF INVENTION: Williams Syndrome Presence or Absence of a LIM-Kinase Gene  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
; STREET: 555 Thirteenth Street, N.W., Suite 701 East  
; CITY: Washington  
; STATE: DC  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/678,039A  
; FILING DATE: 10-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Stephen A.  
; REGISTRATION NUMBER: 38,609  
; REFERENCE/DOCKET NUMBER: 2323-120A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-624-1589  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 792 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-678-039A-40

Query Match 8.0%; Score 72.5; DB 2; Length 792;





REGISTRATION NUMBER: 38,443  
REFERENCE/DOCKET NUMBER: 4600-0124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 853 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-638-911A-25

Query Match 7.5%; Score 68; DB 2; Length 853;  
Best Local Similarity 29.5%; Pred. No. 14;  
Matches 18; Conservative 13; Mismatches 24; Indels 6; Gaps 2;

QY 107 SGPLAMVGSAMMGILLALIEGVIGILLTRYT-----AQOFRNAPPFLEDP-SQLPPKDGDT 160  
DE 748 AGPILMIGLAAGMIYASYTGLSVVVTDMVDVKGKGAPLYRHGDDQATPQPVVQVPPVDHR 807

QY 161 P 161  
DB 808 P 808

RESULT 14  
US-08-638-911A-27  
Sequence 27, Application US/08638911A  
Patent No. 5766916  
GENERAL INFORMATION:  
APPLICANT: Belaeyv, Alexander S.  
APPLICANT: Chong, Susan M.  
TITLE OF INVENTION: Hepatitis G Virus Protease  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/638,911A  
FILING DATE: 04/24/96  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Susan T.  
REGISTRATION NUMBER: 38,443  
REFERENCE/DOCKET NUMBER: 4600-0124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 853 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-638-911A-27

Query Match 7.5%; Score 68; DB 2; Length 853;  
Best Local Similarity 29.5%; Pred. No. 14;  
Matches 18; Conservative 13; Mismatches 24; Indels 6; Gaps 2;

QY 107 SGPLAMVGSAMMGILLALIEGVIGILLTRYT-----AQOFRNAPPFLEDP-SQLPPKDGDT 160

Db 748 AGPILMIGLAAGMIYASYTGLSVVVTDMVDVKGKGAPLYRHGDDQATPQPVVQVPPVDHR 807  
QY 161 P 161  
DB 808 P 808  
RESULT 15  
US-08-638-911A-29  
Sequence 29, Application US/08638911A  
Patent No. 5766916  
GENERAL INFORMATION:  
APPLICANT: Belaeyv, Alexander S.  
APPLICANT: Chong, Susan M.  
TITLE OF INVENTION: Hepatitis G Virus Protease  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/638,911A  
FILING DATE: 04/24/96  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Susan T.  
REGISTRATION NUMBER: 38,443  
REFERENCE/DOCKET NUMBER: 4600-0124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 853 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-638-911A-29

Query Match 7.5%; Score 68; DB 2; Length 853;  
Best Local Similarity 29.5%; Pred. No. 14;  
Matches 18; Conservative 13; Mismatches 24; Indels 6; Gaps 2;

QY 107 SGPLAMVGSAMMGILLALIEGVIGILLTRYT-----AQOFRNAPPFLEDP-SQLPPKDGDT 160  
Db 748 AGPILMIGLAAGMIYASYTGLSVVVTDMVDVKGKGAPLYRHGDDQATPQPVVQVPPVDHR 807  
QY 161 P 161  
DB 808 P 808

Search completed: August 10, 1999, 08:35:21  
Job time: 8700 sec

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